

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model
Run on: January 11, 2003, 06:03:32 ; Search time 6157 Seconds
(without alignments)
11211.930 Million cell updates/sec
Title: US-10-005-344-1
Perfect score: 2372
Sequence: 1 gcaccgcgcgagcttgctg.....attacagcgatgcacccg 2372
Scoring table: OLIGO.NUC
Gapop 60.0 , Gapext 60.0
Searched: 2054640 seqs, 14551402878 residues
Word size : 0
Total number of hits satisfying chosen parameters: 995600
Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
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37: em_hgt_vit:*
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40: em_hgt_mus:*
41: em_hgt_inv:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Summary of results
Length of 100% matches

Result No.	Score	Query Match	Length	ID	Description
1	47	2.0	90	9	HUMDLRFL
2	43	1.8	80	9	HUMDKFAC
3	43	1.8	92	6	AX197472
4	39	1.6	80	9	HUMBRKFA
5	39	1.6	85	6	AR051522
6	39	1.6	85	6	AR072662
7	39	1.6	85	6	AR073207
8	38	1.6	80	9	HUMBRKFA
9	37	1.6	51	6	AX158065
10	37	1.6	51	6	AX161490
11	37	1.6	51	6	AX163420
12	37	1.6	90	9	HUMDLRFL
13	37	1.6	94	6	AX197487
14	36	1.5	51	6	AX161652
15	36	1.5	76	6	A97233
16	35	1.5	40	6	AR208401
17	35	1.5	51	6	AX163202
18	35	1.5	70	9	HSLAS32
19	34	1.4	51	6	AX158807
20	34	1.4	51	6	AX161913
21	34	1.4	54	6	AX322189
22	32	1.3	51	6	AX157145
23	32	1.3	51	6	AX160937
24	32	1.3	92	6	AX197468
25	32	1.3	94	6	AX197476
26	32	1.3	94	6	AX197483
27	31	1.3	66	9	AF087511
28	30	1.3	40	6	A68621
29	30	1.3	51	6	AX156918
30	30	1.3	51	6	AX158063
31	30	1.3	51	6	AX159155
32	30	1.3	51	6	AX190033
33	30	1.3	51	9	S62605
34	30	1.3	100	9	HSU67848
35	29	1.2	29	6	AR208404
36	29	1.2	51	6	AX118161
37	29	1.2	51	6	AX163193
38	29	1.2	51	6	AX163312
39	29	1.2	60	6	AR051487
40	29	1.2	60	6	AR072627
41	29	1.2	60	6	AR073172
42	29	1.2	76	6	AR051499
43	29	1.2	76	6	AR072639
44	29	1.2	76	6	AR073184
45	29	1.2	88	11	HUMDT5056B

ALIGNMENTS

RESULT 1
HUMDLRFL
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

Human low density lipoprotein receptor intron A Alu repeat.
K03555
K03555.1 GI:187104
Alu repeat; low density lipoprotein receptor-1; repeat region.
Human DNA.
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 90)
Lehrman, M.A., Goldstein, J.L., Russell, D.W. and Brown, M.S.
Duplication of seven exons in LDL receptor gene caused by Alu-Alu
recombination in a subject with familial hypercholesterolemia

JOURNAL Cell 48 (5), 827-835 (1987)
MEDLINE 87131094
PUBMED 3815525
COMMENT Clean copy of sequence kindly provided by M.Lehrman (22-APR-1987).
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 /db_xref="taxon:9606"
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HUMBRKFCAC Human alpha-galactosidase breakpoint region. PRI 27-APR-1993
LOCUS Human alpha-galactosidase breakpoint region.
DEFINITION Human alpha-galactosidase breakpoint region.
ACCESSION M36133
VERSION M36133.1 GI:179543
KEYWORDS Fabry disease; breakpoint junction; glycosphingolipid catabolism.
SOURCE Human DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 80)
AUTHORS Kornreich, R., Bishop, D.F. and Desnick, R.J.
TITLE Alpha-galactosidase A gene rearrangements causing Fabry disease.
Identification of short direct repeats at breakpoints in an
Alu-rich gene
JOURNAL J. Biol. Chem. 265 (16), 9319-9326 (1990)
MEDLINE 90264427
PUBMED 2160973
FEATURES
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 Location/Qualifiers
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BASE COUNT 18 a 28 c 17 g 17 t
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Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2330 CCTGGCTCCCAAGTCTGGATTACAGGCATGAGCCACC 2372
Db 17 CCTGGCTCCCAAGTCTGGATTACAGGCATGAGCCACC 59
RESULT 3
AX197472/c
LOCUS AX197472
DEFINITION Sequence 37 from Patent WO0151632.
ACCESSION AX197472
VERSION AX197472.1 GI:15387842
KEYWORDS human.
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 92)
AUTHORS padigar, M., Prayaga, S.K., Taupier, R.J., Mishra, V., Tchernev, V.T.,
Spytek, K.A. and Li, L.

TITLE Odorant receptor polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0151632-A 37 19-JUL-2001;
Curagen Corporation (US)
FEATURES
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Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2319 TGATCGCCACCTCGGCTCCCAAGTCTGGATTACAGGC 2361
Db 59 TGATCGCCACCTCGGCTCCCAAGTCTGGATTACAGGC 17
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HUMBRKFAB Human alpha-galactosidase breakpoint family F. PRI 27-APR-1993
LOCUS Human alpha-galactosidase breakpoint family F.
DEFINITION Human alpha-galactosidase breakpoint family F.
ACCESSION M36132
VERSION M36132.1 GI:179542
KEYWORDS Fabry disease; breakpoint junction; glycosphingolipid catabolism.
SOURCE Human DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 80)
AUTHORS Kornreich, R., Bishop, D.F. and Desnick, R.J.
TITLE Alpha-galactosidase A gene rearrangements causing Fabry disease.
Identification of short direct repeats at breakpoints in an
Alu-rich gene
JOURNAL J. Biol. Chem. 265 (16), 9319-9326 (1990)
MEDLINE 90264427
PUBMED 2160973
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Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2334 GGCCTCCCAAGTCTGGATTACAGGCATGAGCCACC 2372
Db 21 GGCCTCCCAAGTCTGGATTACAGGCATGAGCCACC 59
RESULT 5
AR051522
LOCUS AR051522
DEFINITION Sequence 92 from patent US 5830670.
ACCESSION AR051522
VERSION AR051522.1 GI:5974886
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 85)
AUTHORS de la Monte, S. and Wands, J.R.
TITLE Neural thread protein gene expression and detection of Alzheimer's disease
JOURNAL Patent: US 5830670-A 92 03-NOV-1998;
FEATURES
 source
 1..85
 Location/Qualifiers
 /organism="unknown"
BASE COUNT 13 a 27 c 25 g 20 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 9 GCCAGGATGTCGATCTCCCTGACCTCGTGATCGCGCC 47

RESULT 6
AR072662

LOCUS AR072662 85 bp DNA linear PAT 28-AUG-2000

DEFINITION Sequence 92 from patent US 5948634.

ACCESSION AR072662

VERSION AR072662.1 GI:9999426

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 85)
AUTHORS de la Monte,S. and Wands,J.R.
TITLE Neural Thread protein gene expression and detection of alzheimer's disease

JOURNAL Patent: US 5948634-A 92 07-SEP-1999;
FEATURES Location/Qualifiers
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BASE COUNT 13 a 27 c 25 g 20 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 9 GCCAGGATGTCGATCTCCCTGACCTCGTGATCGCGCC 47

RESULT 7
AR073207

LOCUS AR073207 85 bp DNA linear PAT 28-AUG-2000

DEFINITION Sequence 92 from patent US 5948888.

ACCESSION AR073207

VERSION AR073207.1 GI:9999970

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 85)
AUTHORS de la Monte,S. and Wands,J.R.
TITLE Neural Thread protein gene expression and detection of Alzheimer's disease

JOURNAL Patent: US 5948888-A 92 07-SEP-1999;
FEATURES Location/Qualifiers
source 1..85
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BASE COUNT 13 a 27 c 25 g 20 t

ORIGIN

Query Match 1.6%; Score 39; DB 6; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2290 GCCAGGATGTCGATCTCCCTGACCTCGTGATCGCGCC 2328
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Db 9 GCCAGGATGTCGATCTCCCTGACCTCGTGATCGCGCC 47

LOCUS HUMBKFAA 80 bp DNA linear PRI 27-APR-1993

DEFINITION Human alpha-galactosidase breakpoint region.

ACCESSION M36131

VERSION M36131.1 GI:179541

KEYWORDS Fabry disease; breakpoint junction; glycosphingolipid catabolism.

SOURCE Human DNA.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 80)
AUTHORS Kornreich,R., Bishop,D.F. and Desnick,R.J.
TITLE Alpha-galactosidase A gene rearrangements causing Fabry disease. Identification of short direct repeats at breakpoints in an Alu-rich gene

JOURNAL J. Biol. Chem. 265 (16), 9319-9326 (1990)

MEDLINE 90264427

PUBMED 2160973

FEATURES Location/Qualifiers
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/db_xref="taxon:9606"

BASE COUNT 19 a 28 c 20 g 13 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 9e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2334 GGCCTCCCAAGTCTGGGATTACAGCATGACCCACC 2371
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Db 21 GGCCTCCCAAGTCTGGGATTACAGCATGACCCACC 58

RESULT 9
AX158065

LOCUS AX158065 51 bp DNA linear PAT 22-JUN-2001

DEFINITION Sequence 1393 from Patent WO0140521.

ACCESSION AX158065

VERSION AX158065.1 GI:14539396

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof

JOURNAL Patent: WO 0140521-A 1393 07-JUN-2001;
Curagen Corporation (US)

FEATURES Location/Qualifiers
source 1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"

misc_feature 26

BASE COUNT 9 a 21 c 12 g 9 t

ORIGIN

Query Match 1.6%; Score 37; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.3e-08;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 GTGATCCGCCACCTCGGCTCCCAAGTCTGGGAT 2354
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Db 15 GTGATCCGCCACCTCGGCTCCCAAGTCTGGGAT 51

RESULT 10
AX161490

LOCUS AX161490 51 bp DNA linear PAT 22-JUN-2001

DEFINITION Sequence 4818 from Patent WO0140521.

ACCESSION AX161490
VERSION AX161490.1 GI:14542821
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 4818 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:9606"
misc_feature 26
/note="2 of 2 allelic variants (4817 is other entry)"
BASE COUNT 7 a 22 c 11 g 11 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.3e-08;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2292 CAGGATGCTCGATCTCCTGACCTCGTGATCGGCC 2328
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Db 1 CAGGATGCTCGATCTCCTGACCTCGTGATCGGCC 37
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RESULT 11
AX163420/c
LOCUS AX163420 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6748 from Patent WO0140521.
ACCESSION AX163420
VERSION AX163420.1 GI:14544751
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6748 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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misc_feature 26
/note="2 of 2 allelic variants (6747 is other entry)"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.3e-08;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2318 GGGATCGCCCGACCTCGGCTCCCAAGATGCTGGAT 2354
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Db 37 GGGATCGCCCGACCTCGGCTCCCAAGATGCTGGAT 1
|||||
RESULT 12
HUMDLRM
LOCUS HUMDLRM 90 bp DNA linear PRI 11-JAN-1995
DEFINITION Human low density lipoprotein receptor mutant gene recombination
site.

ACCESSION M15365
VERSION M15365.1 GI:187107
KEYWORDS Alu repeat; LDL receptor; cell surface protein; crossover;
recombination.
SOURCE Human (FH 295) fibroblast DNA, clone p295.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 90)
AUTHORS Lehman,M.A., Goldstein,J.L., Russell,D.W. and Brown,M.S.
TITLE Duplication of seven exons in LDL receptor gene caused by Alu-Alu
recombination in a subject with familial hypercholesterolemia
JOURNAL Cell 48 (5), 827-835 (1987)
MEDLINE 87131094
PUBMED 3815525
COMMENT Clean copy of sequence kindly provided by M.Lehman (22-APR-1987).
Individual FH 295 carries two mutant LDL receptor alleles. The
allele below was inherited from the father and includes a
duplication of exons 2 through 8 that was presumably created by
unequal chromosomal crossover involving Alu repeats in introns 1
and 8. The exact site of recombination cannot be determined
because the sequences of the Alu repeats in introns 1 and 8 of
normal alleles are identical over a span of 26 nucleotides at the
recombination site.
FEATURES
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43..68
/organism="Homo sapiens"
68..>90
/note="LDLR duplicated intron 1 (no splice consensus at
68); putative; does not fit consensus"
BASE COUNT 18 a 33 c 19 g 20 t
ORIGIN 1 bp upstream of NheI site; chromosome 19p13.2-p13.1.
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Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2335 GCCTCCCAAGTCTGGGATTACAGGCATGAGCCACC 2371
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Db 43 GCCTCCCAAGTCTGGGATTACAGGCATGAGCCACC 79
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RESULT 13
AX197487
LOCUS AX197487 94 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 52 from Patent WO0151632.
ACCESSION AX197487
VERSION AX197487.1 GI:15387847
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 94)
AUTHORS Padigaru,M., Prayaga,S.K., Taupier,R.J., Mishra,V., Tchernev,V.T.,
Spytek,K.A. and Li,L.
TITLE Odorant receptor polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0151632-A 52 19-JUL-2001;
Curagen Corporation (US)
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source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 16 a 31 c 26 g 21 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2334 GCCCTCCCAAGTCTGGGATTACAGCATGAGCCAC 2370
|||||
DB 49 GGCCTCCCAAGTCTGGGATTACAGCATGAGCCAC 85

RESULT 14

AX161652/c AX161652 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 4980 from Patent WO0140521.
ACCESSION AX161652
VERSION AX161652.1 GI:14542983
KEYWORDS
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 51)
Shimkets, R.A. and Leach, M.
Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
Patent: WO 0140521-A 4980 07-JUN-2001;
Curagen Corporation (US)
Location/Qualifiers

FEATURES

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/note="2 of 2 allelic variants (4979 is other entry)
Accession number C943979411"

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OY 2335 GCCCTCCCAAGTCTGGGATTACAGCATGAGCCAC 2370
|||||
DB 41 GGCCTCCCAAGTCTGGGATTACAGCATGAGCCAC 6

RESULT 15

A97233 A97233 76 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 79 from Patent WO9918235.
ACCESSION A97233
VERSION A97233.1 GI:6780621
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE

1 (bases 1 to 76)
Abken, H.
PROCESS FOR DETECTING, EXTRACTING OR REMOVING HUMAN OR MAMMALIAN
CELLS WITH A DISTURBED CELLULAR CYCLE REGULATION OR UNLIMITED
PROLIFERATION OR TUMOUR-FORMING ABILITY
Patent: WO 9918235-A 79 15-APR-1999;
ABKEN HINRICH (DE)
Location/Qualifiers

FEATURES

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ORIGIN

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Pred. No. 1.1e-07;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2325 GCCCACCTCGGCTTCCCAAGTCTGGGATTACAGG 2360
|||||
Db 6 GCCCACCTCGGCTTCCCAAGTCTGGGATTACAGG 41

Search completed: January 11, 2003, 08:55:30
Job time : 6160 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: January 11, 2003, 03:27:22 ; Search time 490 Seconds
(without alignments)
10901.510 Million cell updates/sec

Title: US-10-005-344-1
Perfect score: 2372
Sequence: 1 gcacgcgcgacttgctg.....attacagcagcagccaccg 2372

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Searched: 2185239 seqs, 112599159 residues
Word size: 0
Total number of hits satisfying chosen parameters: 2390332

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

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12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
c	1	73	3.1	73	20 AAX35141
	2	60	2.5	20	ABN19842
	3	50	2.1	95	21 AAC28711
	4	47	2.0	47	21 AAZ69526
c	5	46	1.9	95	22 AAK85116
	6	44	1.9	76	21 AAC13689
c	7	42	1.8	87	22 AAL37410
	8	42	1.8	100	22 ABA20222
c	9	41	1.7	86	21 AAC14994

10	40	1.7	99	22	AAK83535	Human immune/haema	
11	40	1.7	99	22	AAK86591	Human immune/haema	
12	39	1.6	99	21	AAC14830	Human secreted pro	
c	13	38	1.6	67	21	AAC14689	Human secreted pro
14	38	1.6	79	21	AAC24033	Human secreted pro	
c	15	38	1.6	98	22	AAK85113	Human immune/haema
16	37	1.6	51	21	AAW77228	Human clone cg4397	
17	37	1.6	51	22	AAI74452	Human silent SNP c	
18	37	1.6	51	22	AAI77877	Human silent SNP c	
c	19	37	1.6	51	22	AAI79807	Human nonconservat
c	20	37	1.6	57	22	AAK83961	Human immune/haema
21	37	1.6	84	21	AAC12517	Human secreted pro	
22	37	1.6	88	22	AAK86579	Human immune/haema	
23	37	1.6	91	22	AAK84173	Human immune/haema	
24	36	1.5	51	21	AAW77000	Human clone cg4294	
c	25	36	1.5	51	22	AAI78039	Human silent SNP c
26	36	1.5	76	20	AAX37046	Human cdc37 nuclei	
c	27	36	1.5	87	22	AAK87262	Human immune/haema
c	28	36	1.5	87	22	AAK87263	Human immune/haema
c	29	36	1.5	100	22	AAK03022	Human reproductive
c	30	36	1.5	100	22	AAK73008	Human immune/haema
31	35	1.5	40	21	AAK97659	Human MDM2 40mer p	
32	35	1.5	40	24	ABL60505	Human MDM2 mRNA fr	
33	35	1.5	51	22	AAI79589	Human silent SNP c	
34	35	1.5	87	22	AAK76817	Human immune/haema	
c	35	35	1.5	100	22	AAK90852	Human digestive sy
36	34	1.4	51	22	AAI75194	Human silent SNP c	
37	34	1.4	51	22	AAI78300	Human silent SNP c	
38	34	1.4	54	24	AAI68926	Activated T-cell d	
39	34	1.4	65	21	AAK12925	Human secreted pro	
c	40	33	1.4	51	22	AAK32116	Human SNP oligonuc
41	32	1.3	51	21	AAW77488	Human Alu subfamll	
c	42	32	1.3	51	22	AAI73532	Human silent SNP c
43	32	1.3	51	22	AAI77324	Human silent SNP c	
44	32	1.3	78	21	AAK11974	Human secreted pro	
45	32	1.3	79	21	AAK12191	Human secreted pro	

ALIGNMENTS

RESULT 1
AAX35141/c
ID AAX35141 standard; DNA; 73 BP.
XX AC AAX35141;
DT 01-JUL-1999 (first entry)
XX DE Nucleotide sequence SEQ ID 49.
XX KW MDM2 protein; antisense oligonucleotide; activator; tumour suppressor;
XX KW inhibition; tumour growth; DNA-damaging agent; camptothecin;
XX KW DNA/RNA hybrid; ss.
XX OS Synthetic.
XX PN W09910486-A2.
XX PD 04-MAR-1999.
XX PF 18-AUG-1998; 98WO-US17147.
XX PR 06-MAY-1998; 98US-0073567.
XX PR 22-AUG-1997; 97US-0916384.
XX (HYBR-) HYBRIDON INC.
XX Agrawal S, Chen J, Zhang R;
XX WPI; 1999-254219/21.
XX New MDM2-specific antisense oligonucleotides

```
xx Disclosure; Page 57; 59pp; English.
xx
xx The specification describes antisense oligonucleotides that
xx inhibits MDM2 protein expression. The antisense oligonucleotides can
xx be used to activate a tumour suppressor. The antisense oligonucleotides
xx are used to inhibit tumour growth in a mammal, including a human,
xx particularly in conjunction with a DNA-damaging agent such as
xx camptothecin. The present sequence appears in the specification.
xx
xx Sequence 73 BP; 17 A; 23 C; 11 G; 22 T; 0 other;
xx
Query Match          3.1%; Score 73; DB 20; Length 73;
Best Local Similarity 100.0%; Pred. No. 5e-25;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 665 AGGTACATCTGTGAGTGAACAGGTGTACCTTGAAGTGGGAGTGATCAAAAGGACCT 724
DB 73 AGGTACATCTGTGAGTGAACAGGTGTACCTTGAAGTGGGAGTGATCAAAAGGACCT 14
QY 725 TGTACAAGAGCTT 737
DB 13 TGTACAAGAGCTT 1
RESULT 2
ABN39842
ID ABN39842 standard; DNA; 60 BP.
XX
XX AC ABN39842;
XX
XX DT 15-JUL-2002 (first entry)
XX
XX DE Human spliced transcript detection oligonucleotide SEQ ID NO:12590.
XX
XX KW Human; mouse; rat; splice transcript; detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200210449-A2.
XX
XX PD 07-FEB-2002.
XX
XX PF 20-JUL-2001; 2001WO-IB01903.
XX
XX PR 28-JUL-2000; 2000US-221607P.
XX
XX PR 02-MAY-2001; 2001US-287724P.
XX
XX PA (COMP-) COMPUGEN INC.
XX
XX PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
XX WPI; 2002-257383/30.
XX
XX PT New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of
XX a genome, useful for detecting tissue-, pathology-, and
XX developmental-specific genes -
XX
XX Example 1; SEQ ID 12590; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises
XX several oligonucleotides, each capable of hybridising selectively to a
XX set of messenger RNAs transcribed from a given transcription unit of
XX the genome, which encodes one or more messenger RNA splice variants.
XX The oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or
XX quantitatively characterising the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal
```

```
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 60 BP; 10 A; 21 C; 16 G; 13 T; 0 other;
XX
```

```
Query Match          2.5%; Score 60; DB 24; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.1e-18;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 98 TGACCGAGATCCTGCTGCTTTGCGACGAGGAGGAGCAGGAGGATGCGGATAGTGCGTA 157
DB 1 TGACCGAGATCCTGCTGCTTTGCGACGAGGAGGAGGAGGATGCGGATAGTGCGTA 60
```

```
RESULT 3
AAC28711
ID AAC28711 standard; cDNA; 95 BP.
XX
XX AC AAC28711;
XX
XX DT 06-OCT-2000 (first entry)
XX
XX DE Human secreted protein 5' EST, SEQ ID NO: 32786.
XX
XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping; ss.
XX
XX OS Homo sapiens.
XX
XX PN EP1033401-A2.
XX
XX PD 06-SEP-2000.
XX
XX PF 21-FEB-2000; 2000EP-0200610.
XX
XX PR 26-FEB-1999; 99US-0122487.
XX
XX PR (GEST ) GENSET.
XX
XX PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
XX WPI; 2000-500381/45.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
XX Claim 1; SEQ ID 32786; 71pp + CD-ROM; English.
XX
```

```
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. NO ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or poly(A)+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
```


CC expression and secretion vectors.

XX Sequence 95 BP; 18 A; 23 C; 26 G; 28 T; 0 other;

XX Query Match 2.1%; Score 50; DB 21; Length 95;
XX Best Local Similarity 100.0%; Pred. No. 7.6e-14;
XX Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2264 AGTAGACAGAGGTTTCACCGTGTAGCCAGGATGCTTCGATCTCCTGA 2313
Db 1 AGTAGACAGAGGTTTCACCGTGTAGCCAGGATGCTTCGATCTCCTGA 50

RESULT 4

AAZ69526

ID AAZ69526 standard; DNA; 47 BP.

XX AC AAZ69526;

DT 10-SEP-2001 (first entry)

XX Human map-related biallelic marker SEQ ID NO:3882.

XX Human genome; biallelic marker; high density disequilibrium map;
XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX haplotyping; hybridisation; identification; characterisation;
XX diagnosis; single nucleotide polymorphism; SNP; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX variation replace(24,T)

XX /*tag= a
XX /standard_name= "single nucleotide polymorphism"

XX WO9954500-A2.

XX PD 28-OCT-1999.

XX XX 21-APR-1999; 99WO-1B00822.

XX PR 21-APR-1998; 98US-0082614.

XX PR 23-NOV-1998; 98US-0109732.

XX XX (GEST) GENSET.

XX XX Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome -

XX Claim 3; Page 1058; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
XX invention, which contain a polymorphic base at position 24 of their
XX nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
XX primers for the biallelic markers. The biallelic markers of the
XX invention have a variety of uses: they can be used for high density
XX mapping of the human genome, and in complex association studies and
XX haplotyping studies which are useful in determining the genetic basis
XX for disease states. Compositions and methods of the invention can also
XX be useful for the identification of the targets for the development of
XX pharmaceutical agents and diagnostic methods, as well as the
XX characterisation of the differential efficacious responses to and side
XX effects from pharmaceutical agents acting on a disease as well as other
XX treatment.

XX N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
XX and 3367, are not actually given a sequence in the Sequence Listing
XX from the present invention.

XX Sequence 47 BP; 8 A; 14 C; 12 G; 13 T; 0 other;

Query Match 2.0%; Score 47; DB 21; Length 47;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-12;
XX Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2271 ACAGGGTTTCACCGTGTAGCCAGGATGCTTCGATCTCCTGACCTC 2317
Db 1 ACAGGGTTTCACCGTGTAGCCAGGATGCTTCGATCTCCTGACCTC 47

RESULT 5

AAK85116/c

ID AAK85116 standard; DNA; 95 BP.

XX AC AAK85116;

DT 07-NOV-2001 (first entry)

XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39928.
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.

XX Homo sapiens.

XX WO200157182-A2.

XX PD 09-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01354.

XX PR 31-JAN-2000; 2000US-0179065.

XX PR 04-FEB-2000; 2000US-0180628.

XX PR 24-FEB-2000; 2000US-0184664.

XX PR 02-MAR-2000; 2000US-0186350.

XX PR 16-MAR-2000; 2000US-0189874.

XX PR 17-MAR-2000; 2000US-0190076.

XX PR 18-APR-2000; 2000US-0198123.

XX PR 19-MAY-2000; 2000US-0205515.

XX PR 07-JUN-2000; 2000US-0209467.

XX PR 28-JUN-2000; 2000US-0214886.

XX PR 30-JUN-2000; 2000US-0215135.

XX PR 07-JUL-2000; 2000US-0216647.

XX PR 11-JUL-2000; 2000US-0216880.

XX PR 11-JUL-2000; 2000US-0217487.

XX PR 14-JUL-2000; 2000US-0218290.

XX PR 26-JUL-2000; 2000US-0220963.

XX PR 26-JUL-2000; 2000US-0220964.

XX PR 14-AUG-2000; 2000US-0224518.

XX PR 14-AUG-2000; 2000US-0224519.

XX PR 14-AUG-2000; 2000US-0225213.

XX PR 14-AUG-2000; 2000US-0225214.

XX PR 14-AUG-2000; 2000US-0225266.

XX PR 14-AUG-2000; 2000US-0225267.

XX PR 14-AUG-2000; 2000US-0225268.

XX PR 14-AUG-2000; 2000US-0225270.

XX PR 14-AUG-2000; 2000US-0225447.

XX PR 14-AUG-2000; 2000US-0225757.

XX PR 14-AUG-2000; 2000US-0225758.

XX PR 18-AUG-2000; 2000US-0225759.

XX PR 22-AUG-2000; 2000US-0226279.

XX PR 22-AUG-2000; 2000US-0226681.

XX PR 22-AUG-2000; 2000US-0226868.

XX PR 22-AUG-2000; 2000US-0227182.

XX PR 23-AUG-2000; 2000US-0227009.

XX PR 30-AUG-2000; 2000US-0228924.

XX PR 01-SEP-2000; 2000US-0229287.

XX PR 01-SEP-2000; 2000US-0229343.

XX PR 01-SEP-2000; 2000US-0229344.

XX PR 01-SEP-2000; 2000US-0229345.

XX PR 05-SEP-2000; 2000US-0229509.

XX PR 05-SEP-2000; 2000US-0229513.

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PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231368.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234397.
PR 26-SEP-2000; 2000US-0234598.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239335.
PR 13-OCT-2000; 2000US-0239337.
PR 20-OCT-2000; 2000US-0240360.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244517.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 17-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX Disclosure; SEQ ID NO 39928; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK62170 to AAK61921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent
CC diseases and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
XX Sequence 95 BP; 19 A; 26 C; 33 G; 17 T; 0 other;
SQ
Query Match 1.9%; Score 46; DB 22; Length 95;
Best Local Similarity 100.0%; Pred. No. 6.9e-12;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2327 CCACCTCGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACCG 2372
Db 54 CCACCTCGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACCG 9
RESULT 6
AAC13689/c
ID AAC13689 standard; cDNA; 76 BP.
XX
AC AAC13689;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 17764.
XX
```

```
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping; ss.
OS Homo sapiens.
XX
XX EPI033401-A2.
PN
XX
XX 06-SEP-2000.
PD
XX
XX 21-FEB-2000; 2000EP-0200610.
XX
XX 26-FEB-1999; 99US-0122487.
PR
XX (GSEST ) GENSET.
FA
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
PI
XX
XX WPI; 2000-500381/45.
DR
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
XX Claim 1: SEQ ID 17764; 71pp + CD-ROM; English.
XX
XX The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.
XX
XX Sequence 76 BP; 19 A; 19 C; 25 G; 13 T; 0 other;
SQ

Query Match 1.9%; Score 44; DB 21; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.5e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2285 TGTATGCCAGGATGCTCGATCTCCCTGACCTCGTATCGGCC 2328
Db 76 TGTATGCCAGGATGCTCGATCTCCCTGACCTCGTATCGGCC 33

RESULT 7
AAL37410/c
ID AAL37410 standard; DNA; 87 BP.
XX
AC AAL37410;
XX
DT 08-JAN-2002 (first entry)
XX
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3775.
XX
XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein;
KW musculoskeletal system; ds.
OS
XX Homo sapiens.
XX
XX WO200155367-A1.
PN
XX
XX 02-AUG-2001.
PD
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17-JAN-2001; 2001WO-US01338.
31-JAN-2000; 2000US-0179065.
04-FEB-2000; 2000US-0180628.
24-FEB-2000; 2000US-0184664.
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01-SEP-2000; 2000US-0229344.
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 PR 20-OCT-2000; 2000US-0241826.
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 PR 05-DEC-2000; 2000US-0256719.
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 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-451937/48.
 DR
 XX

PT Isolated polypeptide for treating, preventing and/or prognosing
 PT disorders related to the musculoskeletal system including
 PT musculoskeletal cancers and also for testing and detection e.g.
 PT diagnosis -
 PS Example 2; SEQ ID NO 3775; 781pp + Sequence Listing; English.
 XX
 XX The invention relates to novel genes (AAL34669-AAL37666) and proteins
 CC (AB03087-AB04109) associated with the musculoskeletal system useful
 CC for preventing, treating or ameliorating medical conditions e.g. by
 CC protein or gene therapy. The genes are isolated from a range of human
 CC tissues disclosed in the specification. The nucleic acids, proteins,
 CC antibodies and (ant)agonists are useful in the diagnosis, treatment
 CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and
 CC other cancers of the adrenal gland, bone, bone marrow, breast,
 CC gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
 CC (c) cardiovascular disorders such as myocardial ischaemia; (d) wound
 CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
 CC and (f) infectious diseases such as viral, bacterial, fungal and
 CC parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 87 BP; 19 A; 23 C; 29 G; 16 T; 0 other;
 SQ
 Query Match 1.8%; Score 42; DB 22; Length 87;
 Best Local Similarity 100.0%; Pred. No. 6.1e-10;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2319 TGATCGCCACCTCGGCTCCAAAGTCTGGGATTACAGG 2360
 Db 48 TGATCGCCACCTCGGCTCCAAAGTCTGGGATTACAGG 7
 RESULT 8
 ABA20222
 ID ABA20222 standard; DNA; 100 BP.
 XX
 XX ABA20222;
 AC
 XX 23-JAN-2002 (first entry)
 DT
 XX Human nervous system related polynucleotide SEQ ID NO 12553.
 DE
 XX Human; neurotropic; cytotropic; cytostatic; dermatological; virucide;
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
 KW antiparkinsonian; antischlicking; antianaemic; antiarthritic; cancer;
 KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
 KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
 KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200159063-A2.
 PN
 XX
 PD 16-AUG-2001.
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 PF 17-JAN-2001; 2001WO-US01334.
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 PR 31-JAN-2000; 2000US-0179065.
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 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
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PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
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PR 11-JUL-2000; 2000US-0217487.
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PR 05-DEC-2000; 2000US-0256719.
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PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-541565/60.
XX
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
XX useful for preventing, diagnosing and/or treating nervous system
XX cancers and metastases -
XX
XX Disclosure; SEQ ID NO 12553; 1701pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (AB11004-ABA21534) and proteins
XX (AB114678-AB18001) useful for preventing, treating or ameliorating
XX medical conditions e.g. by protein or gene therapy. The genes are
XX isolated from a range of human tissues disclosed in the specification.
XX The nucleic acids, proteins, antibodies and (ant)agonists are useful
XX in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast

CC and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 100 BP; 22 A; 30 C; 26 G; 22 T; 0 other;

Query Match 1.8%; Score 42; DB 22; Length 100;
Best Local Similarity 100.0%; Pred. No. 6.1e-10;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2325 GCCACCTCGGCTCCCAAGTGGTGGATTACAGGATGAG 2366
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Db 59 GCCACCTCGGCTCCCAAGTGGTGGATTACAGGATGAG 100

RESULT 9
AAC14994/c
ID AAC14994 standard; cDNA; 86 BP.
XX
AC AAC14994;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 19069.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EPI033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-0200610.
XX
PR 26-FEB-1999; 99US-0122487.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS Claim 1; SEQ ID 19069; 7lpp + CD-ROM; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.

XX
SQ Sequence 86 BP; 24 A; 21 C; 24 G; 17 T; 0 other;

Query Match 1.7%; Score 41; DB 21; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2284 GTGTTAGCCAGGATGCTCGATCTCCCTGACCTCGTGATCC 2324
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Db 62 GTGTTAGCCAGGATGCTCGATCTCCCTGACCTCGTGATCC 22

RESULT 10
AAK83535
ID AAK83535 standard; DNA; 99 BP.
XX
AC AAK83535;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38347.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
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PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0186664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
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PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
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PR 14-AUG-2000; 2000US-0225757.
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PR 01-SEP-2000; 2000US-0229345.

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PR 08-SEP-2000; 2000US-0231124.
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PR 12-SEP-2000; 2000US-0231958.
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PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
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PR 13-OCT-2000; 2000US-0239935.
PR 20-OCT-2000; 2000US-0240960.
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PR 20-OCT-2000; 2000US-0241786.
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PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
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PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246610.
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PR 08-NOV-2000; 2000US-0246611.
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PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.

PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249299.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX
XX Disclosure; SEQ ID NO 38347; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patients own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/hematopoietic-related diseases, especially
XX cancers and cancer metastases of hematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/hematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAK82169
XX represent sequences used in the exemplification of the present invention.
XX
XX Sequence 99 BP; 19 A; 33 C; 27 G; 20 T; 0 other;

Query Match 1.7%; Score 40; DB 22; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.7e-09;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2330 CCTCGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCA 2369
      |||||
Db 60 CCTCGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCA 99

RESULT 11
AAK86591
ID AAK86591 standard; DNA; 99 BP.
XX
XX AAK86591;
AC
XX
XX
DT 07-NOV-2001 (first entry)
XX
```

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41403.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184654.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
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PR 14-AUG-2000; 2000US-0225266.
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PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
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PR 14-AUG-2000; 2000US-0225759.
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PR 05-SEP-2000; 2000US-0229509.
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PR 08-SEP-2000; 2000US-0231242.
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PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
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PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
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PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
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PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 03-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.

PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-483426/52.
DR Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
PT metastasis.
XX
PS Disclosure: SEQ ID NO 41403; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 99 BP; 19 A; 33 C; 27 G; 20 T; 0 other;

Query Match 1.7%; Score 40; DB 22; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.7e-09;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2330 CCTCGGCTCCCAAGTGTGGGATTACAGGCATGAGCCA 2369
|||||
DB 60 CCTCGGCTCCCAAGTGTGGGATTACAGGCATGAGCCA 99
|||||

RESULT 12
AAC14830
ID AAC14830 standard; cDNA; 99 BP.
XX
AC AAC14830;
XX
XX 06-OCT-2000 (first entry)
XX Human secreted protein 5' EST, SEQ ID NO: 18905.
DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping; ss.
KW Homo sapiens.
OS
XX
XX EP1033401-A2.
PN
XX
XX 06-SEP-2000.
PD
XX 21-FEB-2000; 2000EP-0200610.
PF
XX 26-FEB-1999; 99US-0122487.
PR
XX (GEST) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
PI WPI; 2000-500381/45.
XX
XX The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS Claim 1; SEQ ID 18905; 71pp + CD-ROM; English.
XX
XX The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.

XX Sequence 99 BP; 14 A; 33 C; 27 G; 25 T; 0 other;
SQ

Query Match 1.6%; Score 39; DB 21; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2334 GGCCTCCCAAGTGTGGGATTACAGGCATGAGCCACCG 2372
|||||
DB 50 GGCCTCCCAAGTGTGGGATTACAGGCATGAGCCACCG 88
|||||

RESULT 13
AAC14689/c
ID AAC14689 standard; cDNA; 67 BP.
XX
AC AAC14689;
XX
XX 06-OCT-2000 (first entry)
XX Human secreted protein 5' EST, SEQ ID NO: 18764.
DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX Homo sapiens.
OS
XX EP1033401-A2.
PN
XX 06-SEP-2000.
PD
XX 21-FEB-2000; 2000EP-0200610.
PF
XX 26-FEB-1999; 99US-0122487.
PR
XX (GEST) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
PI WPI; 2000-500381/45.
XX
XX The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.

CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.

XX SQ Sequence 67 BP; 17 A; 11 C; 18 G; 21 T; 0 other;

Query Match 1.6%; Score 38; DB 21; Length 67;

Best Local Similarity 100.0%; Pred. No. 5.4e-08; Mismatches 0; Indels 0; Gaps 0;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2328 CACCTCGGCCCTCCCAAGTGTGGGATTACAGGCATGA 2365

DB 66 CACCTCGGCCCTCCCAAGTGTGGGATTACAGGCATGA 29

RESULT 14

AAC24033

ID AAC24033 standard; cDNA; 79 BP.

XX AC AAC24033;

XX DT 06-OCT-2000 (first entry)

XX DE Human secreted protein 5' EST, SEQ ID NO: 28108.

XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX KW gene therapy; chromosome mapping; ss.

XX OS Homo sapiens.

XX PN EP1033401-A2.

XX PD 06-SEP-2000.

XX PF 21-FEB-2000; 2000EP-0200610.

XX PR 26-FEB-1999; 99US-0122487.

XX PA (GST) GENSET.

XX PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX DR WPI; 2000-500381/45.

XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
XX PT diagnostic, forensic, gene therapy and chromosome mapping procedures -

XX PS Claim 1; SEQ ID 28108; 71pp + CD-ROM; English.

XX CC The present sequence is one of a large number of 5' ESTs derived from
XX CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
XX CC identified within the present sequence. The 5' ESTs were prepared from
XX CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
XX CC sequences usually correspond mainly to the 3' untranslated region (UTR)
XX CC of the mRNA because they are often obtained from oligo-dT primed cDNA
XX CC libraries. Such ESTs are not well suited for isolating cDNA sequences
XX CC derived from the 5' ends of mRNAs and even in those cases where longer
XX CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
XX CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
XX CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
XX CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX CC They are used to obtain upstream regulatory sequences and to design
XX CC expression and secretion vectors.

XX SQ Sequence 79 BP; 14 A; 21 C; 18 G; 26 T; 0 other;

Query Match 1.6%; Score 38; DB 21; Length 79;

Best Local Similarity 100.0%; Pred. No. 5.4e-08;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2291 CCAGGATGCTCTCGATCTCCTGACCTCGTGATCGGCC 2328

DB 40 CCAGGATGCTCTCGATCTCCTGACCTCGTGATCGGCC 77

RESULT 15

AAK85113/c

ID AAK85113 standard; DNA; 98 BP.

XX AC AAK85113;

XX DT 07-NOV-2001 (first entry)

XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39925.

XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX KW cytostatic; gene therapy; vaccine; metastasis; ds.

XX OS Homo sapiens.

XX PN WO200157182-A2.

XX PD 09-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01354.

XX PR 31-JAN-2000; 2000US-0179065.

XX PR 04-FEB-2000; 2000US-0180628.

XX PR 24-FEB-2000; 2000US-0184664.

XX PR 02-MAR-2000; 2000US-0186350.

XX PR 16-MAR-2000; 2000US-0189874.

XX PR 17-MAR-2000; 2000US-0190076.

XX PR 18-APR-2000; 2000US-0198123.

XX PR 19-MAY-2000; 2000US-0205515.

XX PR 07-JUN-2000; 2000US-0209467.

XX PR 28-JUN-2000; 2000US-0214886.

XX PR 30-JUN-2000; 2000US-0215135.

XX PR 07-JUL-2000; 2000US-0216647.

XX PR 07-JUL-2000; 2000US-0216880.

XX PR 11-JUL-2000; 2000US-0217487.

XX PR 14-JUL-2000; 2000US-0217496.

XX PR 26-JUL-2000; 2000US-0220963.

XX PR 14-AUG-2000; 2000US-0224518.

XX PR 14-AUG-2000; 2000US-0224519.

XX PR 14-AUG-2000; 2000US-0225213.

XX PR 14-AUG-2000; 2000US-0225214.

XX PR 14-AUG-2000; 2000US-0225266.

XX PR 14-AUG-2000; 2000US-0225267.

XX PR 14-AUG-2000; 2000US-0225268.

XX PR 14-AUG-2000; 2000US-0225270.

XX PR 14-AUG-2000; 2000US-0225447.

XX PR 14-AUG-2000; 2000US-0225757.

XX PR 14-AUG-2000; 2000US-0225758.

XX PR 18-AUG-2000; 2000US-0225759.

XX PR 22-AUG-2000; 2000US-0226279.

XX PR 22-AUG-2000; 2000US-0226681.

XX PR 22-AUG-2000; 2000US-0226688.

XX PR 22-AUG-2000; 2000US-0227182.

XX PR 23-AUG-2000; 2000US-0227009.

XX PR 30-AUG-2000; 2000US-0228924.

XX PR 01-SEP-2000; 2000US-0228927.

XX PR 01-SEP-2000; 2000US-0229343.

XX PR 01-SEP-2000; 2000US-0229344.

XX PR 05-SEP-2000; 2000US-0229345.

XX PR 05-SEP-2000; 2000US-0229509.

XX PR 06-SEP-2000; 2000US-0229513.

XX PR 06-SEP-2000; 2000US-0230437.

PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239335.
PR 13-OCT-2000; 2000US-0239337.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 17-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249219.

PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0256719.
PR 08-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Disclosure; SEQ ID NO 39925; 3071bp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 98 BP; 18 A; 27 C; 36 G; 17 T; 0 other;
Query Match 1.6%; Score 38; DB 22; Length 98;
Best Local Similarity 100.0%; Pred. No. 5.4e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2334 GGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACC 2371
|||||
DB 50 GGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACC 13

Search completed: January 11, 2003, 07:12:37
Job time : 492 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 06:06:17 ; Search time 88 Seconds
(without alignments)
8266.333 Million cell updates/sec

Title: US-10-005-344-1
Perfect score: 2372
Sequence: 1 gaccgcgcagcttgctg.....attacaggcatgagccacg 2372

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA.*
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3: /cgn2_6/prodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/prodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/prodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	73	3.1	73	3	US-09-073-567-49
2	39	1.6	85	2	US-08-454-557C-92
3	39	1.6	85	2	US-08-340-426D-92
4	39	1.6	85	2	US-08-450-673C-92
5	39	1.6	85	5	PCT-US95-17111A-92
6	35	1.5	40	4	US-09-540-699-17
7	30	1.3	40	4	US-09-060-023A-1
8	29	1.2	29	4	US-09-540-699-20
9	29	1.2	60	2	US-08-454-557C-57
10	29	1.2	60	2	US-08-340-426D-57
11	29	1.2	60	2	US-08-450-673C-57
12	29	1.2	60	5	PCT-US95-17111A-57
13	29	1.2	76	2	US-08-454-557C-69
14	29	1.2	76	2	US-08-340-426D-69
15	29	1.2	76	2	US-08-450-673C-69
16	29	1.2	76	5	PCT-US95-17111A-69
17	28	1.2	28	2	US-08-859-998-27
18	28	1.2	28	2	US-08-859-998-28
19	28	1.2	28	4	US-09-225-928-27
20	28	1.2	28	4	US-09-225-928-28
21	28	1.2	28	4	US-09-540-699-16
22	26	1.1	26	4	US-09-280-805-270
23	26	1.1	26	4	US-09-540-699-18
24	26	1.1	35	1	US-08-255-889-10
25	25	1.1	25	4	US-09-280-805-271
26	25	1.1	25	4	US-09-837-149-4
27	25	1.1	75	4	US-09-357-740-14

28	25	1.1	75	4	US-09-357-740-15	Sequence 15, Appl
29	24	1.0	30	4	US-09-480-718-28	Sequence 28, Appl
30	24	1.0	39	4	US-09-480-718-33	Sequence 33, Appl
31	24	1.0	84	2	US-08-454-557C-91	Sequence 91, Appl
32	24	1.0	84	2	US-08-340-426D-91	Sequence 91, Appl
33	24	1.0	84	2	US-08-450-673C-91	Sequence 91, Appl
34	24	1.0	84	5	PCT-US95-17111A-91	Sequence 91, Appl
c 35	23	1.0	23	4	US-09-385-917-4	Sequence 4, Appl
36	23	1.0	30	4	US-09-480-718-35	Sequence 35, Appl
37	23	1.0	36	4	US-09-480-718-34	Sequence 34, Appl
c 38	23	1.0	47	4	US-09-641-638-659	Sequence 659, Appl
39	22	0.9	22	1	US-08-635-820A-1	Sequence 1, Appl
40	22	0.9	22	3	US-09-100-104-1	Sequence 3, Appl
41	22	0.9	22	4	US-09-385-917-3	Sequence 19, Appl
c 42	22	0.9	22	4	US-09-540-699-19	Sequence 31, Appl
43	22	0.9	30	4	US-09-480-718-31	Sequence 28, Appl
c 44	21	0.9	21	1	US-08-753-147-28	Sequence 22, Appl
45	21	0.9	21	3	US-09-073-567-22	

ALIGNMENTS

RESULT 1
US-09-073-567-49/c
; Sequence 49, Application US/09073567
; Patent No. 6013786
; GENERAL INFORMATION:
; APPLICANT: Jlandong Chen
; APPLICANT: Sudhir Agrawal
; APPLICANT: Ruiwen Zhang
; TITLE OF INVENTION: MDM2-SPECIFIC ANTISENSE OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA: US/09/073,567
; APPLICATION NUMBER: US/09/073,567
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Greenfield, Michael S.
; REGISTRATION NUMBER: 37,147
; REFERENCE/DOCKET NUMBER: 98,057-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 913-0001
; TELEFAX: (312) 913-0002
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic acid
; HYPOTHEetical: NO
; ANTI-SENSE: YES
US-09-073-567-49

Query Match 3.1%; Score 73; DB 3; Length 73;
Best Local Similarity 100.0%; Pred. No. 6.7e-24;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 665 AGGTACATCTGTGAGTCAGACAGGTCACCTTGAGGTGGGAGTGATCAAAAGGACCT 724
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US-08-450-673C-92

Query Match 1.6%; Score 39; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2290 GCCAGGATGCTCGATCTCTGACCTCGTGATCGGCC 2328
DB 9 GCCAGGATGCTCGATCTCTGACCTCGTGATCGGCC 47

RESULT 5

PCT-US95-17111A-92
Sequence 92, Application PC/TUS9517111A
GENERAL INFORMATION:
APPLICANT: Wands, Jack R.
APPLICANT: de la Monte, Suzanne
TITLE OF INVENTION: Neural Thread Protein Gene Expression and
TITLE OF INVENTION: Detection of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17111A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 85 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both

PCT-US95-17111A-92

Query Match 1.6%; Score 39; DB 5; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2290 GCCAGGATGCTCGATCTCTGACCTCGTGATCGGCC 2328
DB 9 GCCAGGATGCTCGATCTCTGACCTCGTGATCGGCC 47

RESULT 6

US-09-540-699-17
Sequence 17, Application US/09540699
Patent No. 6383752
GENERAL INFORMATION:
APPLICANT: Agrawal, Sudhir
APPLICANT: Kandimalia, Ekambar R.
TITLE OF INVENTION: Pseudo-Cyclic Oligonucleobases
FILE REFERENCE: 99,128-B
CURRENT APPLICATION NUMBER: US/09/540,699

CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 60/127,138
PRIOR FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: US 60/174,642
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 40
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Oligonucleotide
OTHER INFORMATION: that is complementary to a portion of the human
OTHER INFORMATION: MDM2 mRNA
US-09-540-699-17

Query Match 1.5%; Score 35; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 664 CAGGTACATCTGTGAGTGAGACAGGTGTACCTT 698
DB 6 CAGGTACATCTGTGAGTGAGACAGGTGTACCTT 40

RESULT 7

US-09-060-023A-1/c
Sequence 1, Application US/09060023A
Patent No. 6391642
GENERAL INFORMATION:
APPLICANT: Resnick, Michael A.
APPLICANT: Larionov, Vladimir L.
APPLICANT: Koudrina, Natalay Y.
APPLICANT: Perkins, Edward L.
TITLE OF INVENTION: TRANSFORMATION-ASSOCIATED RECOMBINATION
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Needle & Rosenberg, P.C.
STREET: Suite 1200, 127 Peachtree Street, N.E.
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,023A
FILING DATE: April 14, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11478
FILING DATE: July 9, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perryman, David G.
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 14014.0291
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-0770
TELEFAX: 404-688-9880
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-060-023A-1

Query Match

1.3%; Score 30; DB 4; Length 40;

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Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2332 TCGGCTCCCAAGTCTGGGATTACAGGC 2361
|||||
Db 40 TCGGCTCCCAAGTCTGGGATTACAGGC 11

RESULT 8
US-09-540-699-20/c
; Sequence 20, Application US/09540699
; Patent No. 6383752
; GENERAL INFORMATION:
; APPLICANT: Agrawal, Sudhir
; APPLICANT: Kandimala, Ekambar R.
; TITLE OF INVENTION: Pseudo-Cyclic Oligonucleobases
; FILE REFERENCE: 99,128-B
; CURRENT APPLICATION NUMBER: US/09/540,699
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,138
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/174,642
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: MDM2 mRNA
; OTHER INFORMATION: probe: +338 to +389.
US-09-540-699-20

Query Match 1.2%; Score 29; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.00084;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 649 AGGAATCATCGGACTCAGTACATCTGTG 677
|||||
Db 29 AGGAATCATCGGACTCAGTACATCTGTG 1

RESULT 9
US-08-454-557C-57
; Sequence 57, Application US/08454557C
; Patent No. 5830670
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: Of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,557C
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840003
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TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
US-08-454-557C-57

Query Match 1.2%; Score 29; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACAGGGTTTCACCGTGT 2288
|||||
Db 25 TTTTAGTAGACAGGGTTTCACCGTGT 53

RESULT 10
US-08-340-426D-57
; Sequence 57, Application US/08340426D
; Patent No. 5948634
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: Of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,426D
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
US-08-340-426D-57

Query Match 1.2%; Score 29; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACAGGGTTTCACCGTGT 2288
|||||
Db 25 TTTTAGTAGACAGGGTTTCACCGTGT 53

RESULT 11
US-08-450-673C-57
; Sequence 57, Application US/08450673C
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; Patent No. 5948888
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; NAME: Ludwig, Jack R.
; TITLE OF INVENTION: Neural Thread protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,673C
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609,3840004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; US-08-450-673C-57

Query Match 1.2%; Score 29; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2260 TTTTAGTAGACAGCGGTTTCACCGTGT 2288
Db 25 TTTTAGTAGACAGCGGTTTCACCGTGT 53

RESULT 12
PCT-US95-17111A-57
; Sequence 57: Application PC/TUS9517111A
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; NAME: Ludwig, Jack R.
; TITLE OF INVENTION: Neural Thread protein Gene Expression and
; TITLE OF INVENTION: Detection of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17111A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/340,426
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609,3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; PCT-US95-17111A-57

Query Match 1.2%; Score 29; DB 5; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2260 TTTTAGTAGACAGCGGTTTCACCGTGT 2288
Db 25 TTTTAGTAGACAGCGGTTTCACCGTGT 53

RESULT 13
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; Sequence 69: Application US/08454557C
; Patent No. 5830670
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; NAME: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,557C
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609,3840003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; US-08-454-557C-69

Query Match 1.2%; Score 29; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 0.0008;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2260 TTTTAGTAGACAGCGGTTTCACCGTGT 2288
Db 25 TTTTAGTAGACAGCGGTTTCACCGTGT 53

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Db 25 TTTTAGTAGACAGAGGGTTTCACCGTGT 53

RESULT 14
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; Sequence 69, Application US/08340426D
; Patent No. 5948634
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,426D
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
US-08-340-426D-69

Query Match 1.2%; Score 29; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 0.0008;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2260 TTTTAGTAGACAGAGGGTTTCACCGTGT 2288
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Db 25 TTTTAGTAGACAGAGGGTTTCACCGTGT 53

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Job time : 90 secs

US-08-450-673C-69
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,673C
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
US-08-450-673C-69

Query Match 1.2%; Score 29; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 0.0008;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2260 TTTTAGTAGACAGAGGGTTTCACCGTGT 2288
|||||
Db 25 TTTTAGTAGACAGAGGGTTTCACCGTGT 53

Search completed: January 11, 2003, 08:57:11
Job time : 90 secs

US-08-450-673C-69
; Sequence 69, Application US/08450673C
; Patent No. 5948688
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 06:08:32 ; Search time 108 Seconds
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Perfect score: 2372
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 389086 seqs, 220051671 residues

Word size : 0

Total number of hits satisfying chosen parameters: 239302

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database : Published Applications_NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	43	1-8	92	10	US-09-761-288-37
C 2	42	1-8	87	10	US-09-764-877-3775
C 3	37	1-6	94	10	US-09-761-288-52
C 4	32	1-3	92	10	US-09-761-288-33
C 5	32	1-3	94	10	US-09-761-288-41
C 6	32	1-3	94	10	US-09-761-288-48
C 7	29	1-2	96	10	US-09-761-288-47
C 8	29	1-2	98	10	US-09-764-847-1866
C 9	29	1-2	98	10	US-09-764-847-1867
C 10	28	1-2	28	10	US-09-225-201-27
C 11	28	1-2	28	10	US-09-225-201-28
C 12	28	1-2	84	10	US-09-920-300A-1278
C 13	28	1-2	84	12	US-10-033-528-1278
C 14	28	1-2	88	10	US-09-764-869-1719
C 15	27	1-1	84	10	US-09-764-860-1052
C 16	27	1-1	84	10	US-09-764-860-1053
C 17	27	1-1	87	10	US-09-764-869-1866
C 18	27	1-1	87	10	US-09-764-860-766
C 19	27	1-1	87	10	US-09-764-860-962

C 20	27	1-1	87	10	US-09-764-877-2984
C 21	26	1-1	26	9	US-10-008-922-19
C 22	26	1-1	26	10	US-09-752-983-270
C 23	26	1-1	69	10	US-09-815-343-348
C 24	26	1-1	98	10	US-09-764-860-818
C 25	26	1-1	98	10	US-09-764-860-819
C 26	25	1-1	25	10	US-09-752-983-271
C 27	25	1-1	41	9	US-10-008-922-21
C 28	25	1-1	100	10	US-09-764-860-720
C 29	24	1-0	32	10	US-09-214-371-71
C 30	24	1-0	32	10	US-09-214-371-69
C 31	24	1-0	86	10	US-09-764-887-565
C 32	24	1-0	89	10	US-09-764-887-567
C 33	24	1-0	90	9	US-09-764-904-79
C 34	24	1-0	90	9	US-09-764-904-80
C 35	24	1-0	90	9	US-09-764-904-81
C 36	24	1-0	90	10	US-09-764-860-607
C 37	24	1-0	90	10	US-09-764-860-608
C 38	24	1-0	90	10	US-09-764-860-609
C 39	24	1-0	95	9	US-09-764-868-1444
C 40	24	1-0	96	10	US-09-764-887-554
C 41	24	1-0	100	10	US-09-764-887-560
C 42	24	1-0	100	10	US-09-908-711-136
C 43	24	1-0	100	10	US-09-764-869-1674
C 44	23	1-0	23	10	US-09-884-898-4
C 45	23	1-0	84	10	US-09-764-869-2102

ALIGNMENTS

RESULT 1
US-09-761-288-37/c
; Sequence 37, Application US/09761288
; Patent No. US20020065405A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Taupier, Raymond J
; APPLICANT: Mishra, Vishnu
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberley
; APPLICANT: Li, Li
; TITLE OF INVENTION: NO. US20020065405A1el Polypeptides and Nucleic Acids Encoding
; FILE REFERENCE: 15966-638
; CURRENT APPLICATION NUMBER: US/09761,288
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/177,839
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/176,134
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/175,989
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/218,324
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/220,253
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: 60/178,191
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/178,227
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/220,590
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 92
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-761-288-37
Query Match 1.8%; Score 43; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 5.1e-11;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2319 TGATCCGCCACCTCGGCTCCCAAGTCTGGGATTACAGGC 2361
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Db 59 TGATCCGCCACCTCGGCTCCCAAGTCTGGGATTACAGGC 17

RESULT 2

US-09-764-877-3775/c
; Sequence 3775, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3775
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3775

Query Match 1.8%; Score 42; DB 10; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2319 TGATCCGCCACCTCGGCTCCCAAGTCTGGGATTACAGG 2360
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Db 48 TGATCCGCCACCTCGGCTCCCAAGTCTGGGATTACAGG 7

RESULT 3

US-09-761-288-52
; Sequence 52, Application US/09761288
; Patent No. US20020065405A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Taupier, Raymond J
; APPLICANT: Mishra, Vishnu
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Li, Li
; TITLE OF INVENTION: No. US20020065405A1 Polypeptides and Nucleic Acids Encoding Sam
; FILE REFERENCE: 15966-638
; CURRENT APPLICATION NUMBER: US/09/761,288
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/177,839
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/176,134
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/175,989
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/218,324
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/178,191
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/220,253
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: 60/178,191
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/220,590
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 94
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-761-288-52

Query Match 1.6%; Score 37; DB 10; Length 94;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2334 GGCCTCCCAAGTCTGGGATTACAGGATGAGCCAC 2370
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Db 49 GGCCTCCCAAGTCTGGGATTACAGGATGAGCCAC 85

RESULT 4

US-09-761-288-33/c
; Sequence 33, Application US/09761288
; Patent No. US20020065405A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Taupier, Raymond J
; APPLICANT: Mishra, Vishnu
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Li, Li
; TITLE OF INVENTION: No. US20020065405A1 Polypeptides and Nucleic Acids Encoding
; FILE REFERENCE: 15966-638
; CURRENT APPLICATION NUMBER: US/09/761,288
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/177,839
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/176,134
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/175,989
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/218,324
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/220,253
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: 60/178,191
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/178,227
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/220,590
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 92
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-761-288-33

Query Match 1.3%; Score 32; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2286 GTTAGCCAGGATGGTCTCGATCTCTGACCTC 2317
|||||
Db 92 GTTAGCCAGGATGGTCTCGATCTCTGACCTC 61

RESULT 5

US-09-761-288-41/c
; Sequence 41, Application US/09761288
; Patent No. US20020065405A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Taupier, Raymond J
; APPLICANT: Mishra, Vishnu
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Li, Li
; TITLE OF INVENTION: No. US20020065405A1 Polypeptides and Nucleic Acids Encoding

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; FILE REFERENCE: 15966-638
; CURRENT APPLICATION NUMBER: US/09/761,288
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/177,839
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/176,134
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/175,989
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/218,324
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/220,253
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: 60/178,191
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/178,227
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/220,590
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 94
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-761-288-41

Query Match      1.3%; Score 32; DB 10; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2286 GTTAGCCAGGATGCTCGATCTCTGACCTC 2317
      |||||
DB 94 GTTAGCCAGGATGCTCGATCTCTGACCTC 63

RESULT 6
US-09-761-288-48
; Sequence 48, Application US/09/761,288
; Patent No. US20020065405A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Taupier, Raymond J
; APPLICANT: Mishra, Vishnu
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Li, Li
; TITLE OF INVENTION: No. US20020065405A1 Polypeptides and Nucleic Acids Encoding Sam
; FILE REFERENCE: 15966-638
; CURRENT APPLICATION NUMBER: US/09/761,288
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/177,839
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/176,134
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/175,989
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/218,324
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/220,253
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: 60/178,191
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/178,227
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/220,590
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 96
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-761-288-47

Query Match      1.2%; Score 29; DB 10; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2330 CCTCGCCCTCCCAAGTCTGGATTACA 2358
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DB 50 CCTCGCCCTCCCAAGTCTGGATTACA 22

RESULT 8
US-09-764-847-1866/c
; Sequence 1866, Application US/09/764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
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1

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; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-225-201-28

Query Match          1.2%; Score 28; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1204 CCTAGCTGACTATTGGAATGCACTTC 1231
Db 28 CCTAGCTGACTATTGGAATGCACTTC 1

RESULT 12
US-09-920-300A-1278
; Sequence 1278, Application US/09920300A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547
; CURRENT APPLICATION NUMBER: US/09/920,300A
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 1789
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1278
; LENGTH: 84
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-920-300A-1278

Query Match          1.2%; Score 28; DB 10; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.00096;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2330 CCTCGGCTCCCAAGTCTGGGATTAC 2357
Db 40 CCTCGGCTCCCAAGTCTGGGATTAC 67

RESULT 13
US-10-033-528-1278
; Sequence 1278, Application US/10033528
; Patent No. US20020131971A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547C1
; CURRENT APPLICATION NUMBER: US/10/033,528
; CURRENT FILING DATE: 2001-12-26
; NUMBER OF SEQ ID NOS: 1896
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1278
; LENGTH: 84
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-528-1278

Query Match          1.2%; Score 28; DB 12; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.00096;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2330 CCTCGGCTCCCAAGTCTGGGATTAC 2357
Db 40 CCTCGGCTCCCAAGTCTGGGATTAC 67

US-09-764-869-1719
; Sequence 1719, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1719
; LENGTH: 88
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-1719

Query Match          1.2%; Score 28; DB 10; Length 88;
Best Local Similarity 100.0%; Pred. No. 0.00096;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2330 CCTCGGCTCCCAAGTCTGGGATTAC 2357
Db 61 CCTCGGCTCCCAAGTCTGGGATTAC 88

RESULT 15
US-09-764-860-1052/c
; Sequence 1052, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1052
; LENGTH: 84
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-860-1052

Query Match          1.1%; Score 27; DB 10; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2330 CCTCGGCTCCCAAGTCTGGGATTAC 2356
Db 27 CCTCGGCTCCCAAGTCTGGGATTAC 1

Search completed: January 11, 2003, 08:59:12
Job time : 109 secs
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25

GenCore version 5.1.3
Copyright (C) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 03:15:17 ; Search time 3329 Seconds
(without alignments)
11539.710 Million cell updates/sec

Title: US-10-005-344-1
Perfect score: 2372
Sequence: 1 gcacgcgcgcgttgctg.....attacagcatgagccacgc 2372

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 15154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database :

- EST.*
- 1: em_estba.*
 - 2: em_esthum.*
 - 3: em_estin.*
 - 4: em_estm.*
 - 5: em_estov.*
 - 6: em_estpl.*
 - 7: em_estro.*
 - 8: em_hic.*
 - 9: gb_est1.*
 - 10: gb_est2.*
 - 11: gb_hic.*
 - 12: gb_est3.*
 - 13: gb_est4.*
 - 14: gb_est5.*
 - 15: em_estfun.*
 - 16: em_estom.*
 - 17: gb_gss.*
 - 18: em_gss_hum.*
 - 19: em_gss_inv.*
 - 20: em_gss_pln.*
 - 21: em_gss_vit.*
 - 22: em_gss_fun.*
 - 23: em_gss_mam.*
 - 24: em_gss_mus.*
 - 25: em_gss_other.*
 - 26: em_gss_pro.*
 - 27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	43	1.8	100	13	BC983527 PMO-CN015
C 2	41	1.7	50	9	AU104029 AU104029
C 3	41	1.7	55	10	AW059824 LE8ell.yg
C 4	38	1.6	93	10	AW275505 xno8f10.x
C 5	38	1.6	94	10	AW235474 xnl1f10.x
C 6	37	1.6	37	14	R70733 y146d12.r1

C 7	1.6	80	14	F24490
C 8	1.6	90	17	AZ756775 ex01e07.x
C 9	1.5	54	17	BH70627 LIMGag38
C 10	1.5	61	17	AZ75874 ev10d06.x
C 11	1.5	74	9	AA078709 7T01E11.C
C 12	1.5	59	9	AA082835 zn21g12.s
C 13	1.5	84	10	BE515208 601235919
C 14	1.5	96	9	AA078527 7P05B09.C
C 15	1.4	50	9	AU102534 AU102534
C 16	1.3	72	17	N84707 J0579F.Huma
C 17	1.3	72	17	AQ092880 B06937.r77
C 18	1.3	88	9	AA809831 oa40f11.s
C 19	1.3	96	14	R67088 y130h05.s1
C 20	1.3	50	9	AU103190 AU103190
C 21	1.3	84	14	F34634 HSPD29754.H
C 22	1.3	87	14	T87662 yd91b12.s1
C 23	1.3	100	12	BG099457 naq44d08.
C 24	1.2	97	12	BG152006 naq72f02.
C 25	1.2	100	17	AZ757131 ex05801.r
C 26	1.2	87	9	AA078171 7H15B07.C
C 27	1.1	28	14	R84946 y165g08.r1
C 28	1.1	54	9	AA457759 aa92c06.r
C 29	1.1	62	12	BG527934 602556896
C 30	1.1	62	12	BG776837 602664020
C 31	1.1	62	12	BG777129 602664345
C 32	1.1	72	17	AZ575912 AST-T2200
C 33	1.1	73	9	AA192407 z601a07.r
C 34	1.1	87	10	AA063866 DR0792.KR
C 35	1.1	95	9	AA578401 nl53c01.s
C 36	1.1	34	14	N77004 yv50f05.r1
C 37	1.1	45	9	AA807296 OC37c08.s
C 38	1.1	50	9	AU105707 AU105707
C 39	1.1	87	14	D20989 HUMGS01971
C 40	1.1	100	12	BF675438 602138410
C 41	1.1	32	14	H46868 y019b04.r1
C 42	1.1	40	14	T69198 yc32d04.r1
C 43	1.1	42	9	AA668654 ak49f09.s
C 44	1.1	46	9	AA912807 ol43a05.s
C 45	1.1	78	9	AA047357 zl65h10.r

ALIGNMENTS

RESULT 1
BG983527/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

PMO-CN0155-090301-004-al2 CN0155 Homo sapiens cDNA, mRNA sequence.
EST. 12-JUN-2001

PMO-CN0155-090301-004-al2 CN0155 Homo sapiens cDNA, mRNA sequence.

PMO-CN0155-090301-004-al2 CN0155 Homo sapiens cDNA, mRNA sequence.

PMO-CN0155-090301-004-al2 CN0155 Homo sapiens cDNA, mRNA sequence.

PMO-CN0155-090301-004-al2 CN0155 Homo sapiens cDNA, mRNA sequence.

PMO-CN0155-090301-004-al2 CN0155 Homo sapiens cDNA, mRNA sequence.

PMO-CN0155-090301-004-al2 CN0155 Homo sapiens cDNA, mRNA sequence.

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PMO-CN0155-090301-004-al2 CN0155 Homo sapiens cDNA, mRNA sequence.

PMO-CN0155-090301-004-al2 CN0155 Homo sapiens cDNA, mRNA sequence.

PMO-CN0155-090301-004-al2 CN0155 Homo sapiens cDNA, mRNA sequence.

PMO-CN0155-090301-004-al2 CN0155 Homo sapiens cDNA, mRNA sequence.

PMO-CN0155-090301-004-al2 CN0155 Homo sapiens cDNA, mRNA sequence.

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PMO-CN0155-090301-004-al2 CN0155 Homo sapiens cDNA, mRNA sequence.

PMO-CN0155-090301-004-al2 CN0155 Homo sapiens cDNA, mRNA sequence.

PMO-CN0155-090301-004-al2 CN0155 Homo sapiens cDNA, mRNA sequence.

PMO-CN0155-090301-004-al2 CN0155 Homo sapiens cDNA, mRNA sequence.

PMO-CN0155-090301-004-al2 CN0155 Homo sapiens cDNA, mRNA sequence.

PMO-CN0155-090301-004-al2 CN0155 Homo sapiens cDNA, mRNA sequence.

PMO-CN0155-090301-004-al2 CN0155 Homo sapiens cDNA, mRNA sequence.

PMO-CN0155-090301-004-al2 CN0155 Homo sapiens cDNA, mRNA sequence.

PMO-CN0155-090301-004-al2 CN0155 Homo sapiens cDNA, mRNA sequence.

PMO-CN0155-090301-004-al2 CN0155 Homo sapiens cDNA, mRNA sequence.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 100)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel.: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM04t2-PM0-CN0155-090301-004-a12t3-2001-03-09&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 99.

FEATURES

source
 1..100
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="CN0155"
 /dev_stage="Adult"
 /note="Organ: colon_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 34 a 24 c 22 g 19 t 1 others

BASE COUNT 34 a 24 c 22 g 19 t 1 others

Query Match 1.8%; Score 43; DB 13; Length 100;

Best Local Similarity 100.0%; Pred. No. 6e-08;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2285 TGTAGCCAGGATGCTCGATCCGACCTGCTGATCGGCC 2327

Db 45 TGTAGCCAGGATGCTCGATCCGACCTGCTGATCGGCC 3

RESULT 2
 AUI04029
 LOCUS AUI04029 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 DEFINITION KAIR1572, mRNA sequence.

ACCESSION AUI04029.1 GI:13553550

VERSION EST.

KEYWORDS human.

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 50)

AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata

, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

21270072

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano

, S. Construction and characterization of a full length-enriched and

a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

Enriched cDNA library

Location/Qualifiers

1..50

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="KAIR1572"

/note="Differential display comparison of untreated and

dimethylformate treated U937 cells"

9 a 11 c 16 g 14 t

BASE COUNT 9 a 11 c 16 g 14 t

ORIGIN

Query Match 1.7%; Score 41; DB 9; Length 50;

Best Local Similarity 100.0%; Pred. No. 5.6e-07;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGTTTACCGCTTAGCCAGGATGCTCGATCTCCTGAC 2314

Db 10 GGTTTACCGCTTAGCCAGGATGCTCGATCTCCTGAC 50

RESULT 3

AW059824

LOCUS

DEFINITION

AW059824

VERSION

AW059824.1

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 55)

AUTHORS Brenner, S., Williams, S.R., Vermass, E.H., Storck, T., Moon, K.,

McCollum, C., Mao, J.I., Kirchner, J.J., Eletr, S., DuBridge, R.B.,

Burcham, T. and Albrecht, G.

In vitro cloning of complex mixtures of DNA on microbeads: Physical

separation of differentially expressed cDNAs

Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)

20144098

COMMENT

Contact: Burcham TS

LYNX Therapeutics, Inc.

25861 Industrial Blvd., Hayward, CA 94545, USA

Tel: 510 670 9338

Fax: 510 670 9302

Email: timbelynxgen.com

Sequence obtained from LYNX Therapeutics Megasort technology.

Collected from the down-regulated gate.

High quality sequence stop: 55.

Location/Qualifiers

1..55

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="DNC15"

/cell_type="monocytic leukemia"

/note="Vector: PCR2.1; Cloning of PCR products from

micro-beads carrying 3' end of down-regulated cDNA. THP-1

cells non-induced (treated with DMSO only)."

11 a 19 c 15 g 10 t

BASE COUNT 11 a 19 c 15 g 10 t

ORIGIN

Query Match 1.7%; Score 41; DB 10; Length 55;

Best Local Similarity 100.0%; Pred. No. 5.5e-07;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2320 GATCCGCCACCTCGGCTCCCAAGCTGGGATTACAGG 2360

Db 1 GATCCGCCACCTCGGCTCCCAAGCTGGGATTACAGG 41

RESULT 4

AW275505/c

LOCUS

DEFINITION

AW275505

VERSION

AW275505.1

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 93)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

similar to contains Alu repetitive element; mRNA sequence.

AW275505

93 bp mRNA linear EST 03-JAN-2000

xn08f10.x1 NCI-CGAP_Li5 Homo sapiens cDNA clone IMAGE:2693131 3'

JOURNAL
COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -400P from Gibco.

FEATURES
source

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1. 93
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2693131"
/clone_lib="NCI_CGAP_Li5"
/tissue_type="hepatic adenoma"
/lab_host="DH10B"
/note="Organ: liver; Vector: pCMV-SPORT4; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 0.8 kb."
BASE COUNT      19 a 23 c 23 g 28 t
ORIGIN
```

Query Match 1.6%; Score 38; DB 10; Length 93;

Best Local Similarity 100.0%; Pred. No. 1e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2334 GGCCTCCCAAGTCTGGGATTACAGCATGAGCCACC 2371

Db 78 GGCCTCCCAAGTCTGGGATTACAGCATGAGCCACC 41

RESULT 5
AW235474/C

```
LOCUS      94 bp mRNA linear EST 13-DEC-1999
DEFINITION xnl1f10.x1 NCI_CGAP_Li5 Homo sapiens cDNA clone IMAGE:2693419 3'
            similar to contains Alu repetitive element; mRNA sequence.
ACCESSION  AW235474
VERSION     AW235474.1 GI:6567863
KEYWORDS    EST.
SOURCE      human.
```

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 94)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: polyT not found

Seq primer: -400P from Gibco.

Location/Qualifiers

1. 94

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2693419"

/clone_lib="NCI_CGAP_Li5"

/tissue_type="hepatic adenoma"

/lab_host="DH10B"

FEATURES
source

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1. 94
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2693419"
/clone_lib="NCI_CGAP_Li5"
/tissue_type="hepatic adenoma"
/lab_host="DH10B"
```

/note="Organ: liver; Vector: pCMV-SPORT4; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 0.8 kb."

BASE COUNT 19 a 25 c 20 g 29 t 1 others

ORIGIN

```
Query Match 1.6%; Score 38; DB 10; Length 94;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 2334 GGCCTCCCAAGTCTGGGATTACAGCATGAGCCACC 2371

Db 78 GGCCTCCCAAGTCTGGGATTACAGCATGAGCCACC 41

RESULT 6
R70733

```
LOCUS      37 bp mRNA linear EST 01-JUN-1995
DEFINITION Y146d12.r1 Soares placenta Nb2Hp Homo sapiens cDNA clone
            IMAGE:142295 5' similar to gb:U87914|HUMALNE461 Human carcinoma
            cell-derived Alu RNA transcript, (rRNA); gb:U92424 MDM2 PROTEIN
            (HUMAN); mRNA sequence.
ACCESSION  R70733
VERSION     R70733.1 GI:844250
KEYWORDS    EST.
SOURCE      human.
```

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 37)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 872

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 872 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 1.

Location/Qualifiers

1. 37

/organism="Homo sapiens"

/db_xref="GDB:551330"

/db_xref="taxon:9606"

/clone="IMAGE:142295"

/clone_lib="Soares placenta Nb2HP"

/sex="Female"

/dev stage="Placenta obtained at birth (full term)"

/lab_host="DH10B (ampicillin resistant)"

/note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a

modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dt) primer [5'

AAGTGGAGGATTCGGCGCGAGGAATTTTTTTTTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT7T3 vector. Library

went through one round of normalization. Library

constructed by Bento Soares and M. Fatima Bonaldo.

8 a 11 c 11 g 7 t

BASE COUNT

ORIGIN

```

Query Match          1.6%; Score 37; DB 14; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.7e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2330 CCTCGCCCTCCCAAGTCTGGGATTACAGGCATGAG 2366
      1 CCTCGCCCTCCCAAGTCTGGGATTACAGGCATGAG 37

Db

RESULT 7
F24490/c
LOCUS      F24490      80 bp      mRNA      linear      EST 13-MAY-1999
DEFINITION HSPD10834 HM3 Homo sapiens cDNA clone s4000013A06, mRNA sequence.
ACCESSION  F24490
VERSION    F24490.1 GI:4810116
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 80)
AUTHORS   Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavicini,A.,
            Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valie,G.
TITLE     Identification of 4370 expressed sequence tags from a
            3'-end-specific cDNA library of human skeletal muscle by DNA
            sequencing and filter hybridization
JOURNAL    Genome Res. 6 (1), 35-42 (1996)
MEDLINE    96276048
COMMENT    Contact: Valle G.
            CRIBI Biotechnology Centre
            University of Padua
            Via Trieste 75, 35121 Padua, Italy
            ABI Chromatograms and other information are available on WWW at
            http://group.bio.unipd.it.

FEATURES             source
    source            1..80
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone="s4000013A06"
                        /clone_lib="HM3"
                        /sex="female"
                        /tissue_type="pectoral muscle (after mastectomy)"
                        /note="Vector: pcDNAII (Invitrogen); Site 1: BstXI;
                        Site 2: NotI. The library was constructed by G.
                        Lanfranchi. This library is not subtracted nor normalized.
                        The first strand cDNA was primed with a biotinylated
                        oligo-dT-NotI primer
                        (5'-biotin-AACCGGCTCGAGCGCGCCCTTTTTTTTTTTT-3'). The
                        ds cDNA was sonicated and size-selected in the range
                        350-550 bp. The 3' specific fragments were selected by
                        streptavidin coated magnetic beads, ligated to
                        non-palindromic BstXI adapters, NotI digested and
                        directionally cloned into BstXI-NotI cut pcDNAII vector."

BASE COUNT          18 a 21 c 19 g 22 t
ORIGIN
Query Match          1.6%; Score 37; DB 14; Length 80;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2334 GGCTCCCAAGTCTGGGATTACAGGCATGAGCCAC 2370
      80 GGCTCCCAAGTCTGGGATTACAGGCATGAGCCAC 44

Db

RESULT 8
AZ756775
LOCUS      AZ756775      90 bp      DNA      linear      GSS 01-MAR-2001
DEFINITION ew01e07.x1 PAX3/FKHR CASTING Library 'ew' Homo sapiens genomic
            clone ew01e07 random, DNA sequence.
ACCESSION  AZ756775
VERSION    AZ756775.1 GI:13176230
KEYWORDS   GSS.

SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 90)
AUTHORS   Barber,T.D., Barber,M.C., Tomescu,O., Barr,F.G., Ruben,S. and
            Friedman,T.B.
TITLE     Identification of Target Genes Regulated by PAX3 and PAX3--FKHR in
            Embryogenesis and Alveolar Rhabdomyosarcoma
JOURNAL    Genomics 79 (3), 278-284 (2002)
MEDLINE    21853298
COMMENT    Contact: Friedman TB
            Laboratory of Molecular Genetics
            National Institute on Deafness and Other Communication Disorders,
            National Institute of Health
            5 Research Court, Room 2A-15, Rockville, MD 20850, USA
            Tel: 301 402 7580
            Fax: 301 496 7882
            Email: friedman@nidcd.nih.gov
            Plate: 01 row: e column: 07
            Seq primer: -21M13 forward primer (ABI)
            Class: Random plasmid subclone.
            Location/Qualifiers
                Location            1..90
                source              1..90
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="ew01e07"
                /clone_lib="PAX3/FKHR CASTING Library 'ew'"
                /sex="Male"
                /lab_host="DH10B"
                /note="Vector: pGEM-T Easy; Human genomic DNA was
                partially digested with Sau3AI, ligated to ds linkers,
                and enriched for binding to human PAX3/FKHR protein using
                a whole Genome PCR-based strategy. DNA fragments
                containing putative PAX3/FKHR binding sites were
                amplified by PCR and cloned into pGEM-T Easy (Promega).
                The ligation products were transformed into DH10B
                electrocompetent cells (Life technologies)."
```

best homologue in strain IL1403 is ynbD (46%)

Class: shotgun
High quality sequence start: 30
High quality sequence stop: 54.

FEATURES

source
1. .54
/organism="Lactococcus lactis subsp. cremoris"
/strain="MG1363"
/db_xref="taxon:1359"
/clone_lib="MG1363 Random Sequence Tag Library"
/note="Vector: pSGM2; Site_1: SmaI; Library of chromosomal fragments of L.lactis strain MG1363 was prepared by partial AluI digestion or by sonication."
8 a 16 c 21 g 9 t

BASE COUNT

ORIGIN

Query Match 1.5%; Score 36; DB 17; Length 54;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2337 CTCCTCCAAAGTCTGGGATTACAGCATGAGCCACCG 2372

Db 43 CTCCTCCAAAGTCTGGGATTACAGCATGAGCCACCG 8

RESULT 10

AZ755874

LOCUS

DEFINITION ev10d06.x1 PAX3 CASTing Library 'ev' Homo sapiens genomic clone

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Barber, T.D., Barber, M.C., Tomescu, O., Barr, F.G., Ruben, S. and Friedman, T.B.

TITLE

Identification of Target Genes Regulated by PAX3 and PAX3--FKHR in Embryogenesis and Alveolar Rhabdomyosarcoma

JOURNAL

MEDLINE

COMMENT

Genomics 79 (3), 278-284 (2002)

Contact: Friedman TB
Laboratory of Molecular Genetics
National Institute on Deafness and Other Communication Disorders,
National Institutes of Health
5 Research Court, Room 2A-15, Rockville, MD 20850, USA

Tel: 301 402 7580

Fax: 301 496 7882

Email: friedman@nidcd.nih.gov

Plate: 10 row: d column: 06

Seg primer: -21M13 forward primer (ABI)

Class: random plasmid subclone.

FEATURES

source

1. .61
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ev10d06"
/clone_lib="PAX3 CASTing Library 'ev'"
/sex="Male"
/lab_host="DH10B"

/note="Vector: pGEM-T Easy; Human genomic DNA was partially digested with Sau3AI, ligated to ds linkers, and enriched for binding to human PAX3dQ+ protein using a whole genome PCR-based strategy. DNA fragments containing putative PAX3dQ+ binding sites were amplified by PCR and cloned into pGEM-T Easy (Promega). The ligation products were transformed into DH10B electrocompetent cells (Life Technologies)."

BASE COUNT

ORIGIN

11 a 22 c 16 g 12 t

Query Match

Best Local Similarity 100.0%; Pred. No. 9e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2326 CCCACTCTGGCTCCCAAAGTCTGGGATTACAGGC 2361

Db 18 CCCACTCTGGCTCCCAAAGTCTGGGATTACAGGC 53

RESULT 11

AA078709/c

LOCUS

DEFINITION

7T01E11 Chromosome 7 Thymus cDNA Library Homo sapiens cDNA clone

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Touchman, J.W., Bouffard, G.G., Weintraub, L.A., Idol, J.R., Wang, L.,

Robbins, C.M., Nussbaum, J.C., Lovett, M. and Green, E.D.

2006 expressed-sequence tags derived from human chromosome

7-enriched cDNA libraries

Genome Res. 7 (3), 281-292 (1997)

97228905

Contact: Eric D. Green

Genome Technology Branch

National Human Genome Research Institute/NIH

49 Convent Dr., MSC4431, Building 49, Room 2A08, Bethesda, MD 20892

Tel: 3014020201

Fax: 3014024735

Email: egreen@nhgri.nih.gov

Plate: 01 row: E column: 11

Seg primer: -21M13 (ABI).

Location/Qualifiers

1. .74

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="7T01E11"

/clone_lib="Chromosome 7 Thymus cDNA Library"

/sex="mixture of female and male"

/tissue_type="thymus"

/dev_stage="1 week old (male), 11 year old (female)"

/lab_host="E. coli strain DH5 alpha"

/note="Organ: thymus; Vector: pAMP10; cDNA was generated from cytoplasmic RNA using a mixture of random DNA hexamers and oligo(dT). From this pool of cDNA, human chromosome 7-enriched cDNA was isolated by direct cDNA selection using chromosome 7 genomic DNA (cosmids). The resulting direct-selected cDNA was cloned into a plasmid vector using a non-directional uracil DNA glycosylase (UDG)-mediated cloning strategy."

19 a 17 c 22 g 16 t

BASE COUNT

ORIGIN

Query Match 1.5%; Score 36; DB 9; Length 74;

Best Local Similarity 100.0%; Pred. No. 8.5e-05;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTCTGGGATTACAGGCATGAGCCAC 2370

Db 74 GCCTCCCAAGTCTGGGATTACAGGCATGAGCCAC 39

RESULT 12

AA082835

LOCUS

DEFINITION

zn21912.s1 StrataGene neuroepithelium NT2RAMI 937234 Homo sapiens

cDNA clone IMAGE:548134 3' similar to contains Alu repetitive

59 bp mRNA linear EST 21-OCT-1996

element; mRNA sequence.

AA082835 AA082835.1 GI:1624910

VERSION EST.

KEYWORDS human.

SOURCE

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 59)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,

Chisoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins

,B., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore

,M., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,

Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E.,

Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

97044478

Contact: Wilton RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -40M13 fwd. from AmerSham.

FEATURES

source

1. .59

/organism="Homo sapiens"

/db_xref="GDB:3926650"

/db_xref="taxon:9606"

/clone_lib="IMAGE:548134"

/dev_stage="Ntera-2/RA-MI neuroepithelial cells"

/lab_host="Ntera-2/RA-MI neuroepithelial cells"

/note="Vector: pBluescript SK-; Site:1: EcoRI; Site:2:

XhoI; Cloned unidirectionally. Primer: Oligo dr. NT2

(Ntera-2/cl.D1) precursor cells induced with Retinoic

Acid for 1 week, followed by 3 weeks in mitotic inhibitors

(Replate #2). Average insert size: 1.1 kb; Uni-ZAP XR

Vector; -5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3'

adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

11 a 14 c 16 g 18 t

BASE COUNT

ORIGIN

Query Match 1.5%; Score 35; DB 9; Length 59;

Best Local Similarity 100.0%; Pred. No. 0.00025;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2285 TGTAGCAGGATGCTCGATCTCTGACCTCGT 2319

|||||

Db 25 TGTAGCAGGATGCTCGATCTCTGACCTCGT 59

|||||

RESULT 13

BE515208/c

LOCUS

DEFINITION BE515208 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608045 5',

mRNA sequence.

ACCSSION BE515208

VERSION BE515208.1 GI:9722423

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 84)

NIH-MGC http://mhc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM260 row: e column: 06

High quality sequence stop: 84.

Location/Qualifiers

1. .84

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="IMAGE:3608045"

/clone_lib="NIH_MGC_44"

/tissue_type="endometrium, adenocarcinoma cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: uterus; Vector: pOFB7; Site:1: XhoI; Site:2:

EcoRI; cDNA made by oligo-dr priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCAGG(G). Library constructed by Ling Hong

in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

21 a 21 c 29 g 13 t

BASE COUNT

ORIGIN

Query Match 1.5%; Score 35; DB 10; Length 84;

Best Local Similarity 100.0%; Pred. No. 0.00023;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2290 GCCAGGATGCTCGATCTCTGACCTCGTGATCC 2324

|||||

Db 59 GCCAGGATGCTCGATCTCTGACCTCGTGATCC 25

|||||

RESULT 14

AA078527

LOCUS

DEFINITION AA078527 96 bp mRNA linear EST 24-SEP-1999

7P05B09 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone

7P05B09, mRNA sequence.

ACCSSION AA078527

VERSION AA078527.1 GI:1838015

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 96)

Touchman,O.W., Bouffard,G.G., Weintraub,L.A., Idol,J.R., Wang,L.,

Robbins,C.M., Nussbaum,J.C., Lovett,M. and Green,E.D.

2006 expressed-sequence tags derived from human chromosome

7-enriched cDNA libraries

Genome Res. 7 (3), 281-292 (1997)

97228905

Contact: Eric D. Green

Genome Technology Branch

National Human Genome Research Institute/NIH

49 Convent Dr., MSC4431, Building 49, Room 2A08, Bethesda, MD 20892

Tel: 3014020201

Fax: 3014024735

Email: egreen@nhgri.nih.gov

Plate: 05 row: B column: 09

Seq primer: -21M13 (AB1).

Location/Qualifiers

1. .96

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="IMAGE:3608045"

/clone_lib="Chromosome 7 Placental cDNA Library"

/sex="female"

/dev_stage="placenta obtained at birth (full term)"

/lab_host="E. coli strain DH5 alpha"

FEATURES

source

/note="Organ: placenta; Vector: pAMP10; cDNA was generated from cytoplasmic RNA using a mixture of random DNA hexamers and oligo(dT). From this pool of cDNA, human chromosome 7-enriched cDNA was isolated by direct cDNA selection using chromosome 7 genomic DNA (cosmids). The resulting direct-selected cDNA was cloned into a plasmid vector using a non-directional uracil DNA glycosylase (UDG)-mediated cloning strategy."

BASE COUNT 25 a 29 c 20 g 22 t

ORIGIN

Query Match 1.5%; Score 35; DB 9; Length 96;

Best Local Similarity 100.0%; Pred. No. 0.00022;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2337 CTCCTCAAGTCTGGGATTACAGGCATGAGCCACC 2371

|||||

Db 12 CTCCCAAAGTCTGGGATTACAGGCATGAGCCACC 46

RESULT 15

AU102534

LOCUS

DEFINITION AU102534 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ADSH00605, mRNA sequence.

ACCESSION AU102534

VERSION AU102534.1 GI:13552055

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 50)

AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
Y., Nakamura, Y., Suyama, A. and Sugano, S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale

JOURNAL mapping of mRNA start sites

MEDLINE ENBO Rep. 2 (5), 388-393 (2001)

COMMENT 21270072

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yasukie@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
S. Construction and characterization of a full length-enriched and

a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES Location/Qualifiers

1..50

source /organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="ADSH00605"

/clone_lib="Sugano Homo sapiens cDNA library"

/note="Differential display comparison of untreated and

dimethylfumarate treated U937 cells"

BASE COUNT 10 a 18 c 13 g 9 t

ORIGIN

Query Match 1.4%; Score 34; DB 9; Length 50;

Best Local Similarity 100.0%; Pred. No. 0.00074;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2330 CTCGGCTCCCAAAGTCTGGGATTACAGGCAT 2363

|||||

Db 10 CCTCGGCTCCCAAAGTCTGGGATTACAGGCAT 43

Search completed: January 11, 2003, 07:04:15

Job time : 3334 secs

